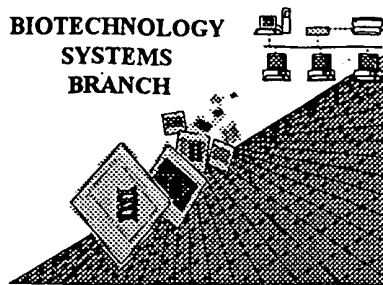


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,823
Source: Pat/1/p
Date Processed by STIC: 1/10/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/efs/downloads/documents.htm>> , EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/009,823

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/009,823

DATE: 01/10/1
TIME: 13:14:3

Input Set: J009823.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Agriculture Victoria Services Pty Ltd AND Australian Pork Limited
2 Pfizer Products Inc.
3 <120> TITLE OF INVENTION: Lawsonia ^{derived} gene and related FlgE polypeptides, (pep)?
4 their uses. *see item 2 on*
5 <130> FILE REFERENCE: *Error summary sheet*
6 <140> CURRENT APPLICATION NUMBER: US/10/009,823
7 <141> CURRENT FILING DATE: 2001-11-12
8 <150> EARLIER APPLICATION NUMBER: US 60/133,973
9 <151> EARLIER FILING DATE: 1999-05-12
10 <160> NUMBER OF SEQ ID NOS: 6
11 <170> SOFTWARE: PatentIn Ver. 2.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 502
14 <212> TYPE: PRT
15 <213> ORGANISM: Lawsonia intracellularis
16 <400> SEQUENCE: 1
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18 1 5 10 15
19 Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile
20 20 25 30
21 Gly Tyr Lys Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp
22 35 40 45
23 Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met
24 50 55 60
25 Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe
26 65 70 75 80
27 Glu Pro Gly Asn Ser Val Thr Asp Leu Ala Ile Gly Gly Lys Gly Phe
28 85 90 95
29 Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn
30 100 105 110
31 Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr
32 115 120 125
33 Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr
34 130 135 140
35 Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser
36 145 150 155 160
37 Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp
38 165 170 175
39 Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu
40 180 185 190
41 Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr
42 195 200 205
43 Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His
44 210 215 220

Does Not Comply
Corrected Diskette Needed

see pp 4-5, too

W-*OK*

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/10/009,823

DATE: 01/10/
TIME: 13:14:

Input Set: J009823.RAW

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45   Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys
46   225                      230                      235                      240
47   Thr Phe Glu Tyr Leu Val Ala Met Asn Pro Ser Glu Asp Gly Ser Ala
48                      245                      250                      255
49   Ala Ser Gly Thr Asp Ser Ala Gly Leu Leu Met Ser Gly Thr Met Thr
50                      260                      265                      270
51   Phe Ser Ser Asn Gly Glu Leu Lys Asn Met Thr Ala Phe Thr Pro Thr
52                      275                      280                      285
53   Gly Ser Ala Thr Lys Asp Leu Asn Ala Trp Gln Pro Ala Pro Leu Val
54                      290                      295                      300
55   Asn Gly Leu Pro Gln Phe Ser Ala Asn Phe Val Gly Ala Gly Ile Gln
56   305                      310                      315                      320
57   Pro Leu Thr Leu Asp Phe Gly Ile Lys Ser Gln Gln Asn Met Trp Ala
58                      325                      330                      335
59   Gly Ala Pro Ala Ser Ala Ala Ala Ile Gly Thr Asp Ile Gly Lys Leu
60                      340                      345                      350
61   Pro Ser Met Met Pro Ile Gln Thr Ser Ser Gly Asn Ser Thr Ala Arg
62                      355                      360                      365
63   Asn Gly Ser Ser Ser Thr Arg Arg Tyr Ser Gln Asp Gly Tyr Pro Gln
64                      370                      375                      380
65   Gly Asp Leu Val Asp Val Thr Ile Thr Ser Glu Gly Lys Leu Gln Gly
66   385                      390                      395                      400
67   Lys Tyr Ser Asn Ser Gln Val Val Asp Phe Tyr Asn Ile Pro Leu Ala
68                      405                      410                      415
69   Arg Phe Thr Ser Glu Asp Gly Leu Arg Arg Glu Gly Asn Asn His Tyr
70                      420                      425                      430
71   Ser Ala Thr Leu Asp Ser Gly Gly Pro Glu Phe Gly Leu Pro Gly Thr
72                      435                      440                      445
73   Ser Asn Tyr Gly Lys Leu Ser Val Asn Gln Leu Glu Thr Ser Asn Val
74                      450                      455                      460
75   Asp Met Ser Arg Glu Met Val Asn Met Ile Ile Ile Gln Arg Gly Phe
76   465                      470                      475                      480
77   Gln Met Asn Ser Lys Ser Val Thr Thr Ala Asp Thr Met Leu Gln Lys
78                      485                      490                      495
79   Ala Leu Glu Leu Lys Arg
80                      500

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81 <210> SEQ ID NO 2
82 <211> LENGTH: 1509
83 <212> TYPE: DNA
84 <213> ORGANISM: Lawsonia intracellularis
85 <220> FEATURE:
86 <221> NAME/KEY: CDS
87 <222> LOCATION: (1)..(1506)
88 <400> SEQUENCE: 2

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89   atg atg ggg agt ttg ttt att ggt gca aca ggt atg aaa acc cat agt   48
90   Met Met Gly Ser Leu Phe Ile Gly Ala Thr Gly Met Lys Thr His Ser
91       1                      5                      10                      15
92   aca ggg ttg ggt act gtc tcc aat aat att gct aac gca aat acc att   96
93   Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile
94                      20                      25                      30

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RAW SEQUENCE LISTING PATENT APPLICATION US/10/009,823

DATE: 01/10/2002
TIME: 13:14:31

Input Set: J009823.RAW

95	ggg tat aag cag caa cag gta gtg ttt caa gac ctg ttt agt caa gat	144
96	Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp	
97	35 40 45	
98	tta gca ata ggt tct act gga agt cag ggg cca aac cag gct ggt atg	192
99	Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met	
100	50 55 60	
101	gga gca cag gtt gga agt gtt cgc aca att ttt aca cag ggt gct ttt	240
102	Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe	
103	65 70 75 80	
104	gaa cct ggc aat agt gta aca gat ctt gct att ggt gga aaa ggt ttt	288
105	Glu Pro Gly Asn Ser Val Thr Asp Leu Ala Ile Gly Gly Lys Gly Phe	
106	85 90 95	
107	ttt cag gtt aca tta gag gat aaa gta cac tat aca cga gca ggg aat	336
108	Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn	
109	100 105 110	
110	ttt cgt ttt act caa gat ggt ttt tta aat gat cct agc gga ttt act	384
111	Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr	
112	115 120 125	
113	tta atg ggc tca aga ata tct aat aat cct aac ata aaa aag gaa acc	432
114	Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr	
115	130 135 140	
116	ctt gaa cca att cag tta gac ttt aat gat cct aca gta gca aag tct	480
117	Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser	
118	145 150 155 160	
119	cct gca aaa aca agt aca gca tta aac gct gtg gta aac ctt ggt gat	528
120	Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp	
121	165 170 175	
122	agt aca gat aaa aca caa agt gaa gct aat cca tac ttt gca ctt ctt	576
123	Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu	
124	180 185 190	
125	gag agc tgg aaa gga aat gga aca cct cct att tct aca tca aac tac	624
126	Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr	
127	195 200 205	
128	tca tat gca caa cct atg aga gta tat gat caa caa gga aat tct cac	672
129	Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His	
130	210 215 220	
131	gat ata act gta tat ttt gat gga gca ccc tct tca aca gga agt aaa	720
132	Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys	
133	225 230 235 240	
134	aca ttt gaa tac ctt gta gct atg aat cct agt gaa gat gga agt gct	768
135	Thr Phe Glu Tyr Leu Val Ala Met Asn Pro Ser Glu Asp Gly Ser Ala	
136	245 250 255	
137	gca tca gga aca gat agt gca ggt ctc tta atg tct gga act atg aca	816
138	Ala Ser Gly Thr Asp Ser Ala Gly Leu Leu Met Ser Gly Thr Met Thr	
139	260 265 270	
140	ttt tca agt aat ggc gaa tta aaa aat atg aca gct ttt act cct act	864
141	Phe Ser Ser Asn Gly Glu Leu Lys Asn Met Thr Ala Phe Thr Pro Thr	
142	275 280 285	
143	ggc tct gca aca aaa gat tta aat gca tgg caa cca gca cca tta gtc	912
144	Gly Ser Ala Thr Lys Asp Leu Asn Ala Trp Gln Pro Ala Pro Leu Val	

PAGE: 4

RAW SEQUENCE LISTING PATENT APPLICATION US/10/009,823

DATE: 01/10/
TIME: 13:14:

Input Set: J009823.RAW

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145          290          295          300
146    aat ggt tta cca cag ttt tca gca aat ttt gtt ggt gca gga ata cag    960
147    Asn Gly Leu Pro Gln Phe Ser Ala Asn Phe Val Gly Ala Gly Ile Gln
148    305          310          315          320
149    cct tta aca tta gac ttt gga att aaa agc caa cag aat atg tgg gca    1008
150    Pro Leu Thr Leu Asp Phe Gly Ile Lys Ser Gln Gln Asn Met Trp Ala
151    325          330          335
152    gga gct cca gca tcc gct gct gcc ata ggt aca gat att ggg aaa ttg    1056
153    Gly Ala Pro Ala Ser Ala Ala Ala Ile Gly Thr Asp Ile Gly Lys Leu
154    340          345          350
155    cca tca atg atg cca ata caa aca tcc agc ggt aat tct aca gca aga    1104
156    Pro Ser Met Met Pro Ile Gln Thr Ser Ser Gly Asn Ser Thr Ala Arg
157    355          360          365
158    aat gga tca tct tca aca aga aga tat agc caa gat ggt tat cct cag    1152
159    Asn Gly Ser Ser Ser Thr Arg Arg Tyr Ser Gln Asp Gly Tyr Pro Gln
160    370          375          380
161    gga gat cta gta gat gtc aca att acc tct gaa ggg aaa tta caa ggt    1200
162    Gly Asp Leu Val Asp Val Thr Ile Thr Ser Glu Gly Lys Leu Gln Gly
163    385          390          395          400
164    aag tat agt aat agt cag gtt gtt gat ttt tat aat att cct tta gca    1248
165    Lys Tyr Ser Asn Ser Gln Val Val Asp Phe Tyr Asn Ile Pro Leu Ala
166    405          410          415
167    cgc ttt aca agt gag gat gga tta aga cga gaa ggg aat aac cat tat    1296
168    Arg Phe Thr Ser Glu Asp Gly Leu Arg Arg Glu Gly Asn Asn His Tyr
169    420          425          430
170    tcc gca aca ctt gac tca ggt ggg cca gag ttt gga ttg cca gga aca    1344
171    Ser Ala Thr Leu Asp Ser Gly Gly Pro Glu Phe Gly Leu Pro Gly Thr
172    435          440          445
173    tct aac tat gga aaa ctt agt gtg aat caa ctt gag act tct aac gta    1392
174    Ser Asn Tyr Gly Lys Leu Ser Val Asn Gln Leu Glu Thr Ser Asn Val
175    450          455          460
176    gac atg agc aga gaa atg gtt aat atg att att att caa cgt ggt ttt    1440
177    Asp Met Ser Arg Glu Met Val Asn Met Ile Ile Ile Gln Arg Gly Phe
178    465          470          475          480
179    cag atg aat agt aaa tct gtt aca aca gca gac aca atg cta caa aaa    1488
180    Gln Met Asn Ser Lys Ser Val Thr Thr Ala Asp Thr Met Leu Gln Lys
181    485          490          495
182    gca ctt gaa cta aag cgt taa    1509
183    Ala Leu Glu Leu Lys Arg
184    500
185    <210> SEQ ID NO 3
186    <211> LENGTH: 21
187    <212> TYPE: DNA
188    <213> ORGANISM: Artificial Sequence
189    <220> FEATURE:
190    <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
191    <400> SEQUENCE: 3
192    ctatttttag gagatgttat c
193    <210> SEQ ID NO 4
194    <211> LENGTH: 22

```

*Insufficient exploration -
give
source
of genetic
material
(see item 11 on Enol
Summary Sheet*

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/009,823DATE: 01/10/
TIME: 13:14:3

Input Set: J009823.RAW

195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: *same error*
199 <400> SEQUENCE: 4
200 tacaaaaatta acaataaaaat ac
201 <210> SEQ ID NO 5
202 <211> LENGTH: 38
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
207 <400> SEQUENCE: 5
208 gcgaattcca tatgatgggg agtttggtta ttggtgcc
209 <210> SEQ ID NO 6
210 <211> LENGTH: 40
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
215 <400> SEQUENCE: 6
216 gctctagaga ctagtcatat taacgcttta gttcaagtgc

22

38

see item 9 on Error Summary Sheet

40

Input Set: J009823.RAW

Line ? Error/Warning

Original Text

5 W Response to "File Reference" is Missing
208 W "N" or "Xaa" used: Feature required

<130>
gcgaattcca tatgatgggg agtttggtta ttgntgcc